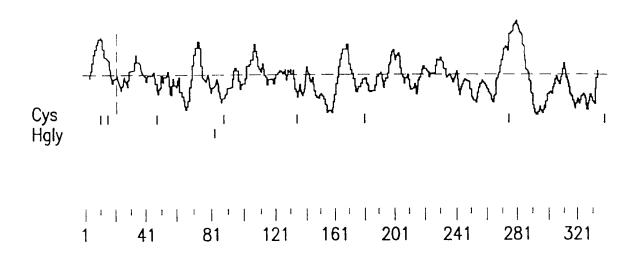
Р Р Μ Τ F C 11 GGAGTCGACCCACGCGTCCGCAGGGCTGAGGAACC ATG TCT CCA TCC CCG ACC GCC CTC TTC TGT CTT 68 Р Р R V Α Q S G Ρ K S L Q 31 GGG CTG TGT CTG GGG CGT GTG CCA GCG CAG AGT GGA CCG CTC CCC AAG CCC TCC CTC CAG 128 S Р Ε Р L Κ ٧ T L R Q G 51 GCT CTG CCC AGC TCC CTG GTG CCC CTG GAG AAG CCA GTG ACC CTC CGG TGC CAG GGA CCT 188 Ε Κ L S S S R L R Υ Q 71 CCG GGC GTG GAC CTG TAC CGC CTG GAG AAG CTG AGT TCC AGC AGG TAC CAG GAT CAG GCA 248 Κ R S L G Υ R Α Μ Α R S Υ 91 GTC CTC TTC ATC CCG GCC ATG AAG AGA AGT CTG GCT GGA CGC TAC CGC TGC TCC TAC CAG 308 Р S D 0 L S Ε L V Α T G V 111 AAC GGA AGC CTC TGG TCC CTG CCC AGC GAC CAG CTG GAG CTC GTT GCC ACG GGA GTT TTT 368 S 0 Р G Р Α S S Α G G D 131 GCC AAA CCC TCG CTC TCA GCC CAG CCC GGC CCG GCG GTG TCG TCA GGA GGG GAC GTA ACC 428 0 R Υ G F D Q F Υ Ε Α L Κ D 151 CTA CAG TGT CAG ACT CGG TAT GGC TTT GAC CAA TTT GCT CTG TAC AAG GAA GGG GAC CCT 488 Υ K Р Ε R W Υ R Α S F Ρ Α Ν Ι Ι T ٧ 171 GCG CCC TAC AAG AAT CCC GAG AGA TGG TAC CGG GCT AGT TTC CCC ATC ATC ACG GTG ACC 548 S F S G Τ Υ R C Y S S R Р Y 191 Α Α Н D GCC GCC CAC AGC GGA ACC TAC CGA TGC TAC AGC TTC TCC AGC AGG GAC CCA TAC CTG TGG 608 S Р Α S D Р Ε Ĺ V V T G T S V T 211 TOG GOO COO AGO GAO COO CTG GAG CTT GTG GTC ACA GGA ACC TOT GTG ACC COO AGO CGG 668 T S S V Ε F S Ε T 231 Α Α TTA CCA ACA GAA CCA CCT TCC TCG GTA GCA GAA TTC TCA GAA GCC ACC GCT GAA CTG ACC 728 F T T Ε 251 T V T S S I Τ GTC TCA TTC ACA AAC AAA GTC TTC ACA ACT GAG ACT TCT AGG AGT ATC ACC ACC AGT CCA 788 Y 271 را CAD CAG TAC TAC ACC AAG GGU AAG CTG DIY 848 291 G A 7 APA APA DIEG GCG GGG TITE OTG SOA GAG GAG EGG 908 \Box \Box \mathbb{Z} Α V 0 E 311 R CAC AGO CGG AGG AAG CGT OTHE ORGERNAL AGES GOT AGES GAG AGG COG OFF COG COC 968

TG.1A

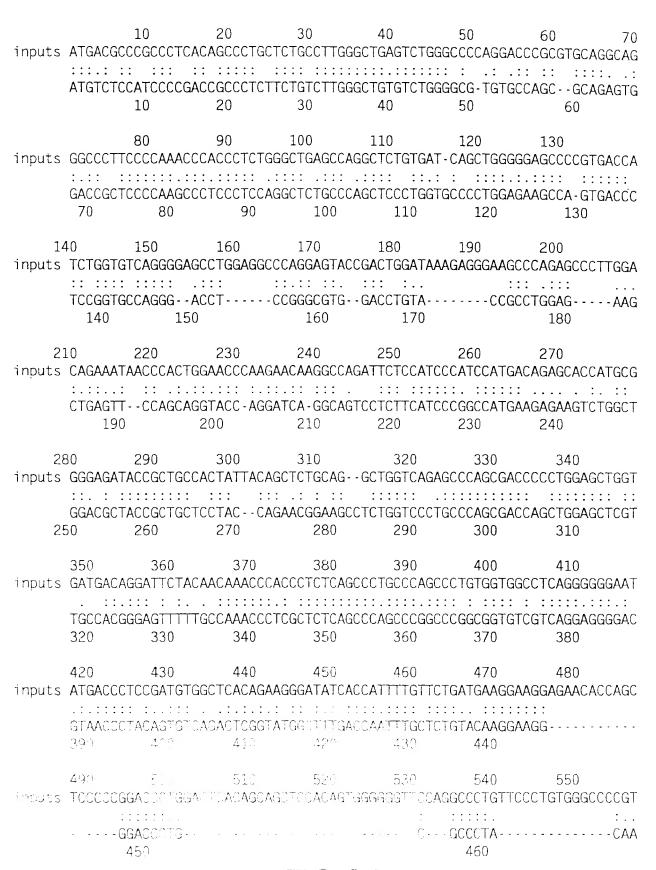
S Ţ R Κ Н 331 CTG CCG CCC CTC CCG CAG ACC CGG AAA TCA CAC GGG GGT CAG GAT GGA GGC CGA CAG GAT 1028 С 340 GTT CAC AGC CGC GGG TTA TGT TCA TGA 1055 CCGCTGAACCCCAGGCACGGTCGTATCCAAGGGAGGGATCATGGCATGGGAGGCGACTCAAAGACTGGCGTGTGTGGAG 1134 CGTGGAAGCAGGAGGCAGAGGCTACAGCTGTGGAAACGAGGCCATGCTGCCTCCTGGTGTTCCATCAGGGAGCCG 1213 AATATGGGCTCCAGACGGATCTCTAAGGTTCCCAGCTCTCAGGGTTGACTCTGTTCCATCCTCTGTGCAAAATCCTCCT 1450 GTGCTTCCCTTTGGCCCTCTGTGCTCTTGTCTGGTTTTCCCCAGAAACTCTCACCCTCACTCCATCTCCCACTGCGGTC 1529 AGCACGTTGCCCGCTTCCCTTCACATTAGAAAACAAGATCAGCCTGTGCAACATGGTGAAACCTCATCTCTACCAACAA 1687 AACAAAAAAACACAAAAATTAGCCAGGTGTGGTGGTGCATCCCTATACTCCCAGCAACTCGGGGGGCTGAGGTGGGAGA 1766 ATGGCTTGAGCCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATCACACCACTGCACTCTAGCTCGGGTGACGAAGCCTGA 1845 CCTTGTCTCAAAAAATACAGGGATGAATATGTCAATTACCCTGATTTGATCATAGCACGTTGTATACATGTACTGCAAT 1924 AAAAAAAAAAAAAAGGGCGGGCCGCTAGACTAGTCTAGAGAACA 2047

FIG.1B



MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLE KLSSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP GPAVSSGGDVTLQCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPIITVTAAHSGTYRC YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT TETSRSITTSPKESDSPAGPARQYYTKGNLVRICLGAVILIILAGFLAEDWHSRRKRLRH RGRAVQRPLPPLPQTRKSHGGQDGGRQDVHSRGLCS

FIG.2



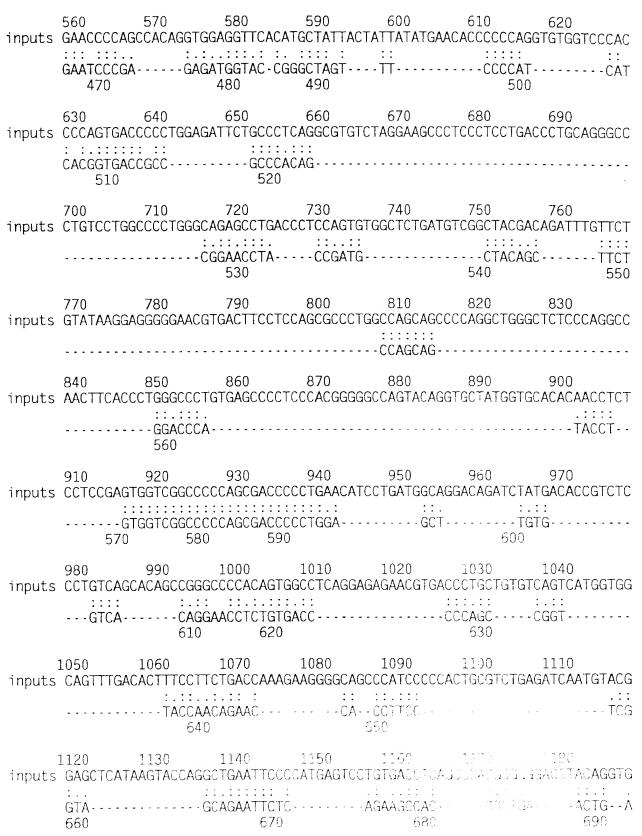


FIG.3B

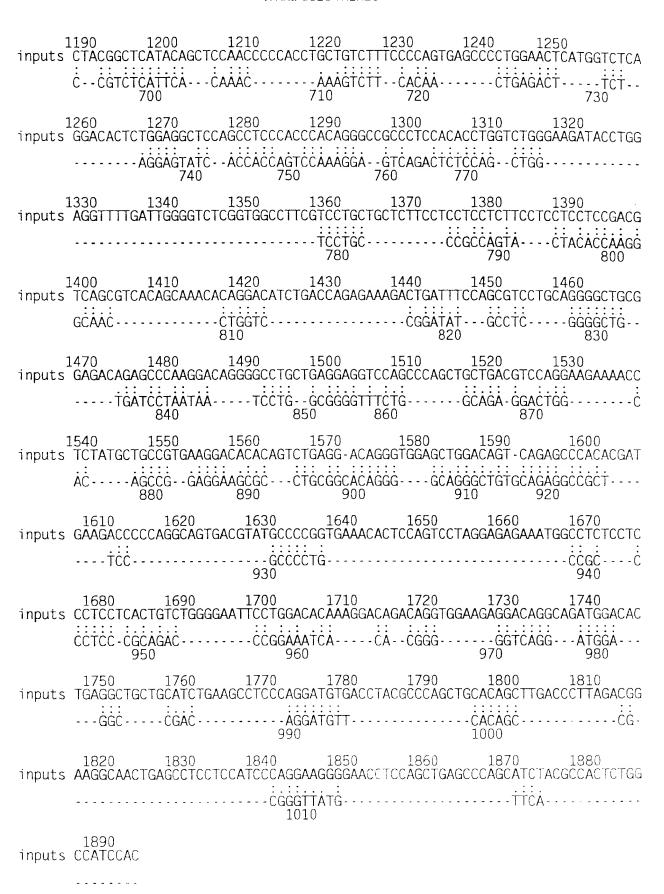
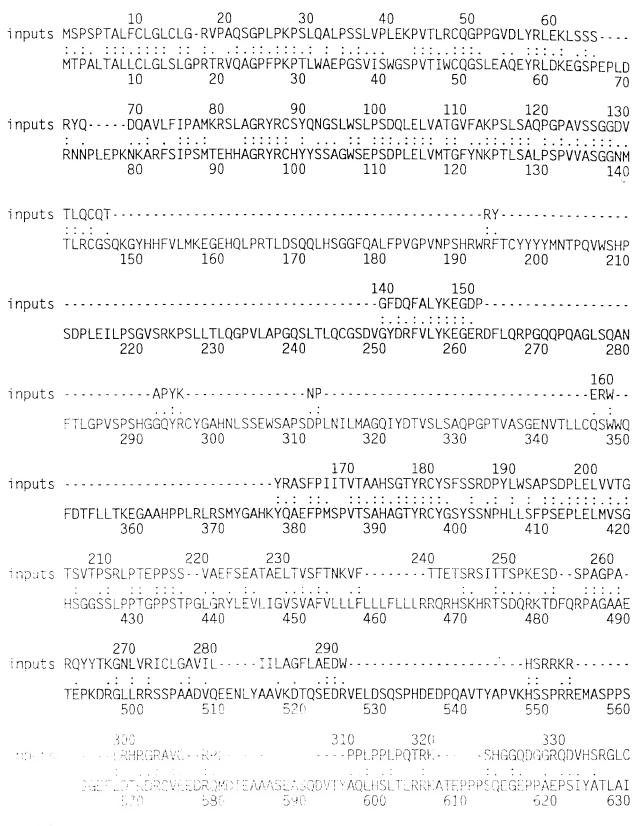


FIG.3C



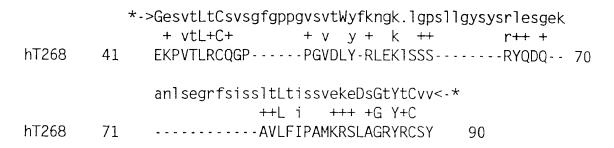


FIG.5A

*->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
G++vtL+C+++ + ++ y k+g++ + y+++
hT268 127 GGDVTLQCQTR---YGFDQFALY-KEGDpAP----YKNPERWYR-- 162

anlsegrfsissltLtissvekeDsGtYtCvv<-*
++++i++v++ sGtY+C
hT268 163 -------ASFPIITVTAAHSGTYRCYS 182

FIG.5B

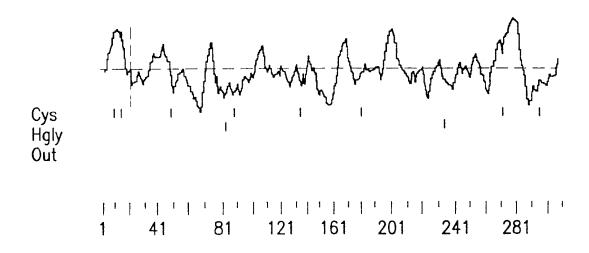
GAGTCGACCCACGCGTCCGCTTCCCTGCTTGGCCACATAGCTCAGGACTGGGTTGCAGAACC ATG TCT CCA GCC 74 F C Ι G C ٧ Q ٧ Ι Q T 24 TCA CCC ACT TTC TTC TGT ATT GGG CTG TGT GTA CTG CAA GTG ATC CAA ACA CAG AGT GGC 134 Р Q Α Q S S 44 CCA CTC CCC AAG CCT TCC CTC CAG GCT CAG CCC AGT TCC CTG GTA CCC CTG GGT CAG TCA 194 С G Р Р D V D 0 L Υ R L Ε К L 64 GTT ATT CTG AGG TGC CAG GGA CCT CCA GAT GTG GAT TTA TAT CGC CTG GAG AAA CTG AAA Ε D 0 D F F Ι Р Τ Ε М R 84 CCG GAG AAG TAT GAA GAT CAA GAC TIT CTC TTC ATT CCA ACC ATG GAA AGA AGT AAT GCT 314 S Υ Q Ν G S Η W S 1 S 104 GGA CGG TAT CGA TGC TCT TAT CAG AAT GGG AGT CAC TGG TCT CTC CCA AGT GAC CAG CTT 374 S Τ ٧ Υ Α K Α Н Ρ S Α 124 GAG CTA ATT GCT ACA GGT GTG TAT GCT AAA CCC TCA CTC TCA GCT CAT CCC AGC TCA GCA 434 R Τ Κ С 0 S Υ S F 144 GTC CCT CAA GGC AGG GAT GTG ACT CTG AAG TGC CAG AGC CCA TAC AGT TTT GAT GAA TTC 494 K Ε G D Τ G Р Υ Κ R Р Ε Κ W Υ 164 GTT CTA TAC AAA GAA GGG GAT ACT GGG CCT TAT AAG AGA CCT GAG AAA TGG TAC CGG GCC T S G Τ Y R Ι V Τ Α Α Н C Y 184 AAT TTC CCC ATC ATC ACA GTG ACT GCT GCT CAC AGT GGG ACG TAC CGG TGT TAC AGC TTC 614 Α Р Р 204 TCC AGC TCA TCT CCA TAC CTG TGG TCA GCC CCG AGT GAC CCT CTA GTG CTT GTG GTT ACT 674 T S 0 Р Τ F F S F Р Τ 224 GGA CTC TCT GCC ACT CCC AGC CAG GTA CCC ACG GAA GAA TCA TTT CCT GTG ACA GAA TCC 734 Р S T Ţ T 244 N K I Ε Κ TCC AGG AGA CCT TCC ATC TTA CCC ACA AAC AAA ATA TCT ACA ACT GAA AAG CCT ATG AAT 794 Р Р 264 Ι G F ATC ACT GCC TCT CCA GAG GGG CTG AGC CCT CCA ATT GGT TTT GCT CAT CAG CAC TAT GCC 854 C G 284 R Ι L Α Т Ι Ι Ι T G AAG GGG AAT CTG GTC CGG ATA TGC CTT GGT GCC ACG ATT ATA ATA ATT TTG TTG GGG CTT 914 C 304 R Κ Κ R L Q H M R Α CTA GCA GAG GAT TGG CAC AGT CGG AAG AAA TGC CTG CAA CAC AGG ATG AGA GCT TTC CAA 974 Р Р 314 AGG CCA CTA CCA CCC CTC CCA CTG GCC TAG 1004

GGACATACTCAAGAGTGGGGAGGTTATATAAAAAAAATGAGTGTGGAGAATAAATGCAGAGCCAACAAGGTGAAAAAAA 1162

Α

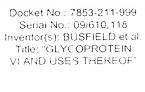
1163

AAATAACTTGGCTTTCAGCAGAGGGATTGACCAGACATCCATGCACAACCATGGACATCACCACTAGAGCCACAGACAT 1083



MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRL EKLKPEKYEDQDFLFIPTMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAH PSSAVPQGRDVTLKCQSPYSFDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAAHSGTYR CYSFSSSSPYLWSAPSDPLVLVVTGLSATPSQVPTEESFPVTESSRRPSILPTNKISTTE KPMNITASPEGLSPPIGFAHQHYAKGNLVRICLGATIIIILLGLLAEDWHSRKKCLQHRM RALQRPLPPLPLA

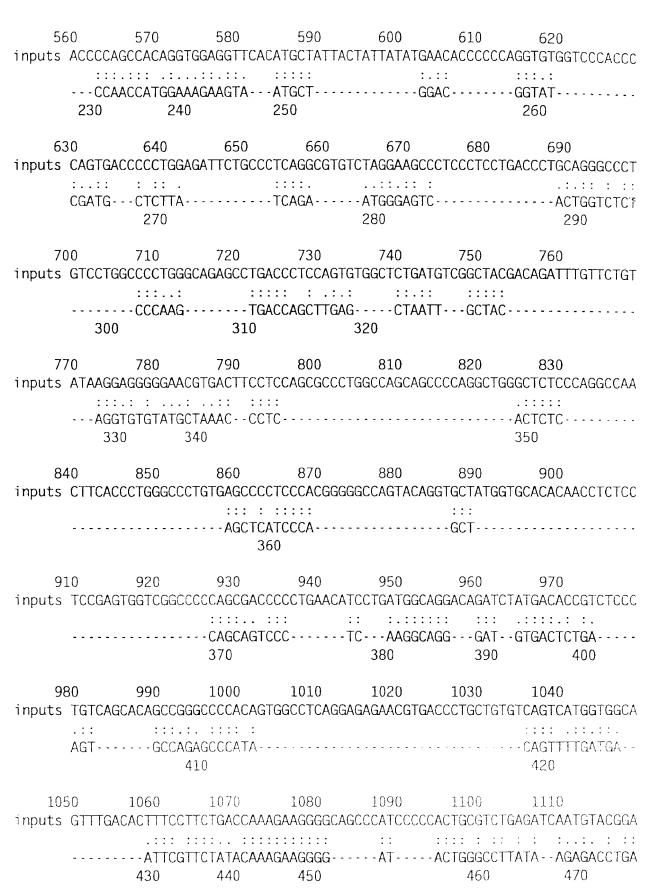
FIG.7



				30				70
inputs				TCTGCCTTGGG		GCCCCAGGAC	CCGCGTGC	AGGCAG
				.:: ::: ACTTTCTT				
		.0		20	30			
	1	.0		20	30			
	8	30	90	100	110	120	130	140
inputs	GGCCCTTCC	CCAAACCC	ACCCTCTG	GGCTGAGCCAG	GCTCTGTGAT	CAGCTGGGG	AGCCCCGT	GACCAT
					::::			
			TG	GGCTG		CTGC		
					40			
	1 F	;n	160	170	180	190	200	210
inputs				CAGGAGTACCG				
трасс	0144.470			: . : . : . : :		::.:		:::
		. 		- AAGTGATCC -		AAACA	CAGAG	-TGG
				50		60		70
	0.0	20	220	240	250	200	270	200
innute				240 ACAAGGCCAGA				
mpucs				::::			AUAGCACCA	rideda
				-CAAG				
			80		90			
				310				
inputs			TATTACAG	CTCTGCAGGCT				aGIGAI
	:)	: :.::: `TCAGCC			:::. :: CAGTTCC	CTG-GTACCC	::::: CTGGGTCA	: 3
		100			110	120		4
	•							
				380				
inputs	GACAGGAT	TCTACAACA	VAACCCACC	CTCTCAGCCCT	GCCCAGCCCT	GTGGTGGCCT	CAGGGGGG.	AATATG
	.::: :	: : . :				:.::::::::::::::::::::::::::::::::::::		
		IAIIC			140		150	-
	130				140		130	
	4	130	440	450	460	470	480	
inputs				GGATATCACCA				CAGCTC
·				:::::::::::::::::::::::::::::::::::::::				
				THATATOGOCH			. (1)	
	160)	ì	.7(30 19	(1)		
1	an i	500	510	520	436	540	550	
				TCCACAGTGGG				CCGTGA
	:::::			:::::::::::::::::::::::::::::::::::::::				
				AGTATG				-CATT-
				200	210	220		

FIG. 8A

Title: "GLYCOPROTEIN VI AND USES THEREOF"



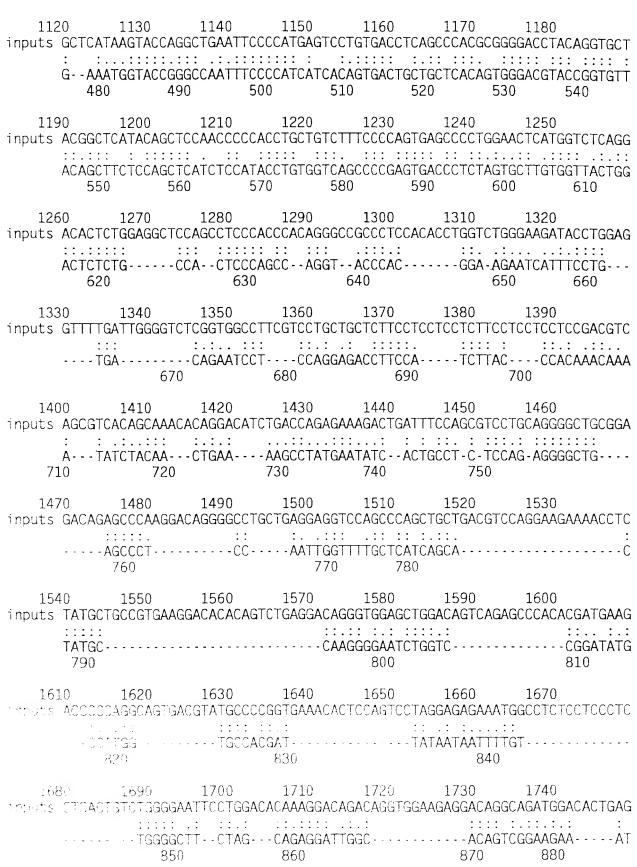


FIG.8C

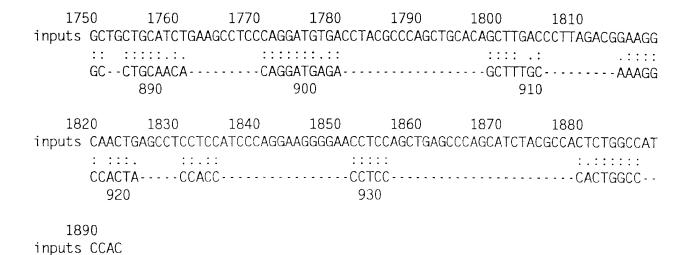


FIG. 8D



inputs A

	*->	>GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek G+sv L+C+ ++v y + k ++ +++e +							
mT268	42	GQSVILRCQGPPDVDLY-RLEK1KPEKYEDQ 71							
anlsegrfsissltLtissvekeDsGtYtCvv<-*									
mT268	72	DFLFIPTMERSNAGRYRCSY 91							

FIG.10A

	*.	->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek	
		G +vtL C++ ++ y k+g++ + Y+r+e +	
mT268	128	GRDVTLKCQSPYSFDEFVLY-KEGDtGPYKRPEKW-Y 16	2
		anlsegrfsissltLtissvekeDsGtYtCvv<-*	
		+ ++i++v++ sGtY+C	
mT268	163	RANFPIITVTAAHSGTYRCYS 183	

FIG.10B

		10	20	36	40	50	60	
inputs	MSPSPTAL	FCLGLCLGR	V-PAQSGPL	PKPSLQALPS	GLVPLEKPVTL	RCQGPPGVDL	YRLEKLSSSF	RYQD
	:::		:					:.:
	MSPASPTI				CLVPLGQSVII			
		10	20	30		50	60	70
	70	80	90	100	110	120	130	
inputs	QAVLFIP	AMKRSLAGRY	RCSYQNGSL	WSLPSDQLEL	VATGVFAKPSI	_SAQPGPAVSS	SGGDVTLQCQ	TRYG
	:. :::: ODFLFIP	.: :: :::: TMERSNAGRY	:::::: RCSYQNGSH	::::::::::::::::::::::::::::::::::::::	: ::: ::: :ATGVYAKPSI	:::::: _SAHPSSAVP(: :::::: GRDVTLKCQS	:: SPYS
	7	80			110	120	130	140
14	40	150	160	170	180	190	200	
inputs	FDQFALY	KEGDPAPYKN	PERWYRASF	PIITYTAAMS	GTYRCYSFSSI	RDPYLWSAPSI	OPLELVVTGTS	SVTP
			::.::::::::::::::::::::::::::::::::::::	:::::				
	FDEFVLY	KEGDTGPYKR	PEKWYRANF	PIITYTAAHS	GTYRCYCESS:	SSPYLWSAPSE	OPLVLVVTGLS	SATP
		150	160	170	180	190	200	210
2:	10	220	230	240	250	260	270 🕈	
inputs	SRLPTEP	PSSVAEFSEA	TAELTVSFT	NEVETTETSR	SITTOPKESO	SPAGPARQY ^v	TRIGNLVRICLO	IVAE
	::::	:.::						: : : :
	SQVPTEE:	SEPVTEDSEF	:PSILPT		METACPEGLO	PPIGFAHQHYA	ALGNLVRICL(EATI
		220	230	240	250	260	270	
7)	80	290	300	310	321	330		
	~ ~				PQTRESHGGQ		SLCS	
прас	LITEMU		TILITING O	QIVI ELLER E	, gritishaaq	Budingo mon	3 200	
	: IIII GL	 LΔEDWH GRYK	CLOHRME AL	Ur ol bol o .	 		.	
	280	290	300	310				

FIG. 11

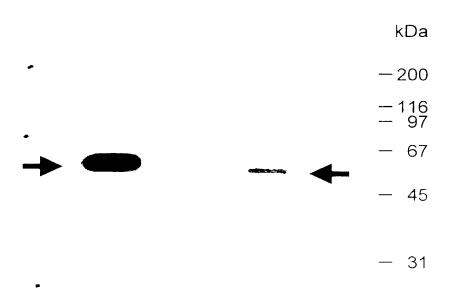


FIG.12

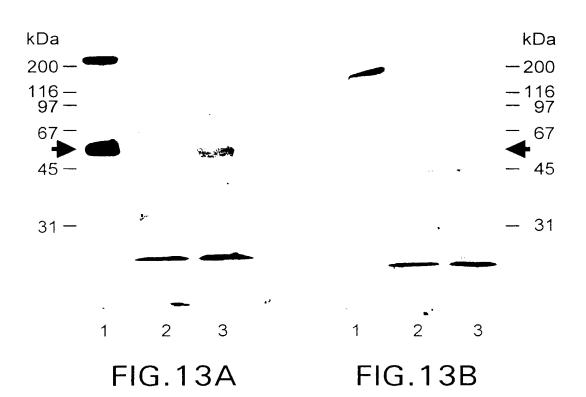




FIG.14A



FIG.14B

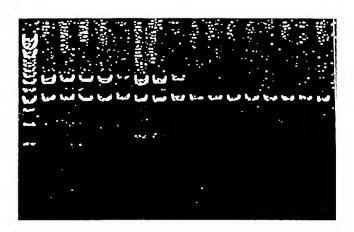


FIG.14C

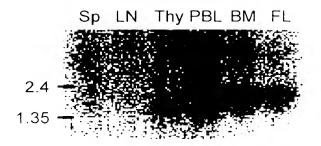
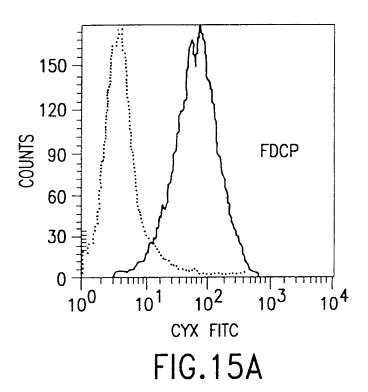
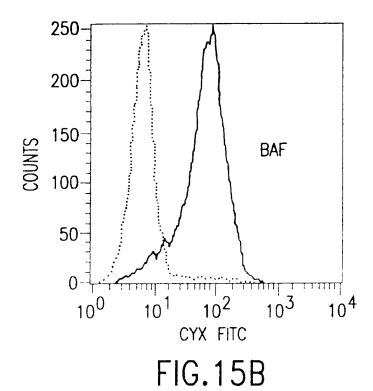
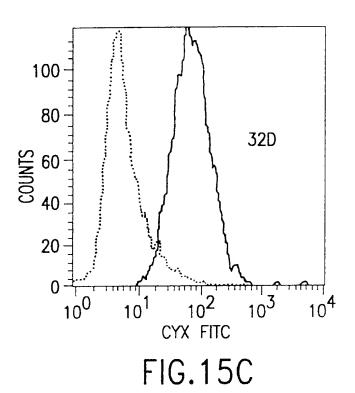
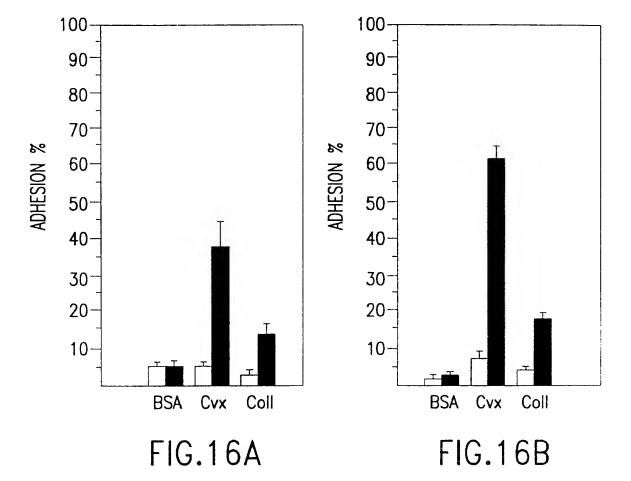


FIG.14D

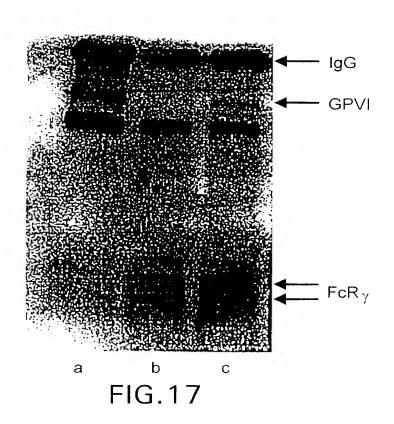


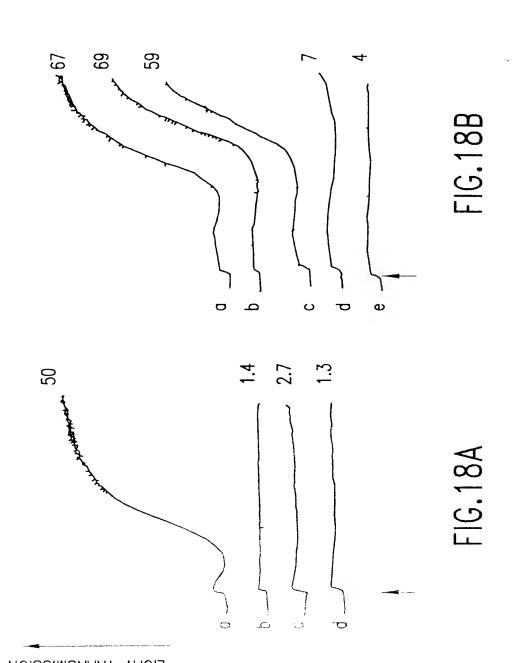






Serial No.: 09/610,118 Inventor(s): BUSFIELD et al. Title: "GLYCOPROTEIN VI AND USES THEREOF"





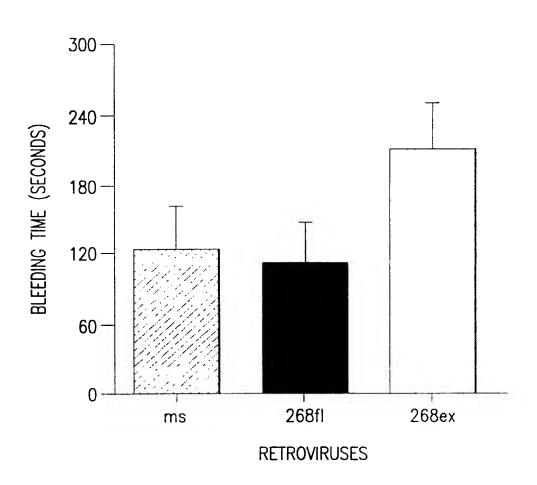


FIG.19

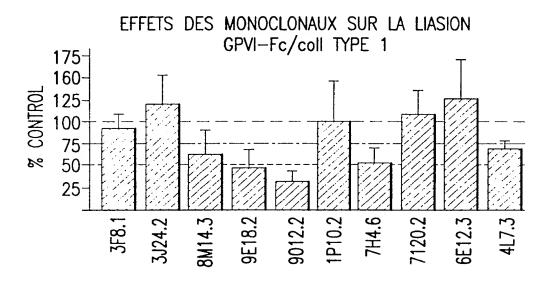
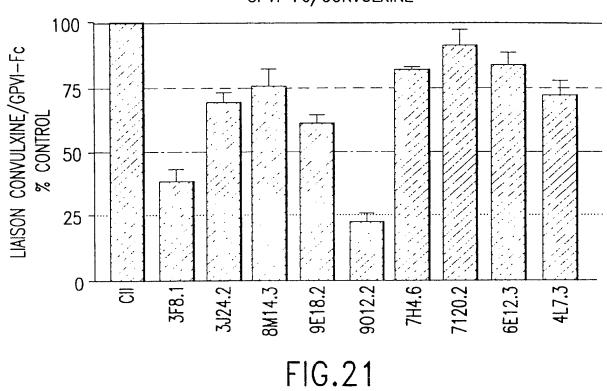


FIG.20

EFFET DES MONOCLONAUX SUR LA LIAISON GPVI-Fc/CONVULXINE



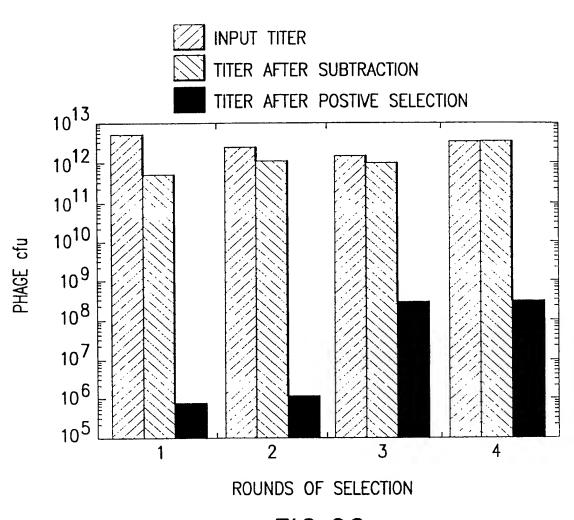


FIG.22

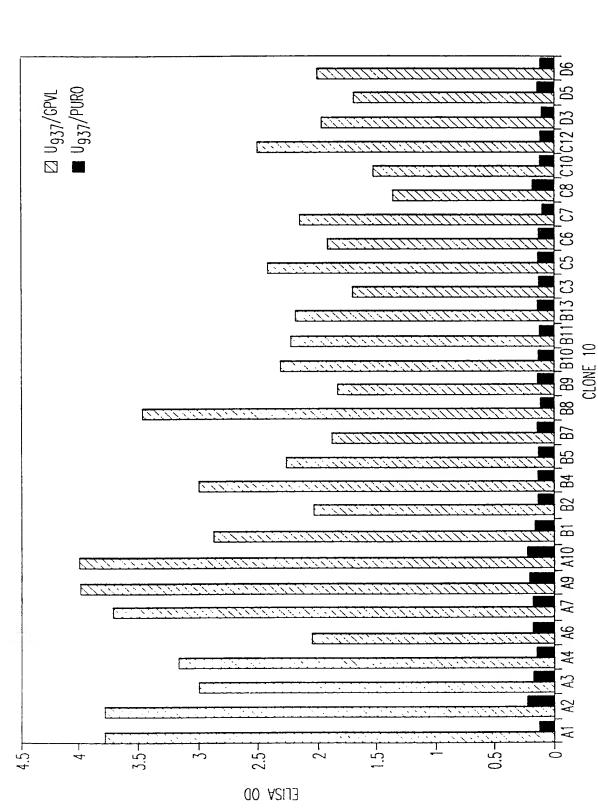


FIG.23A

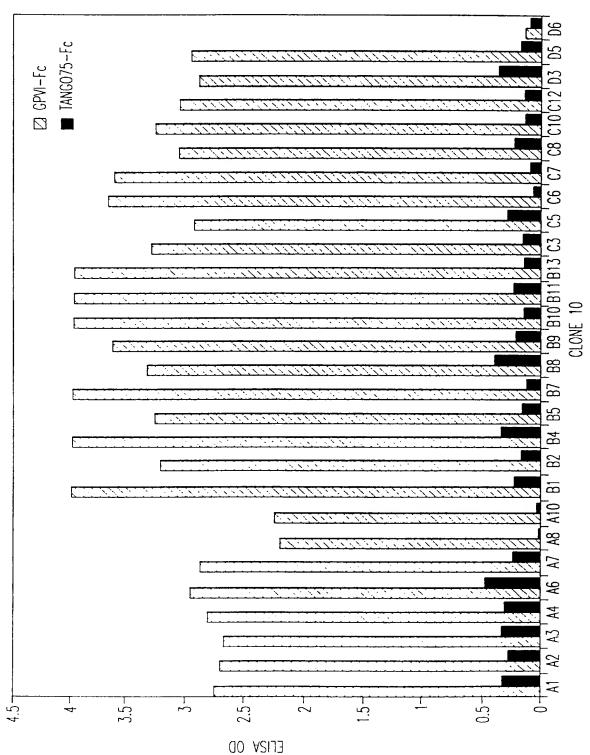


FIG.23E

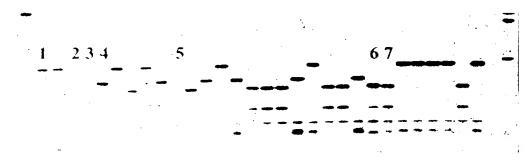
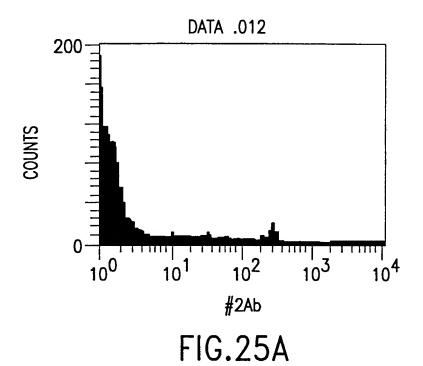
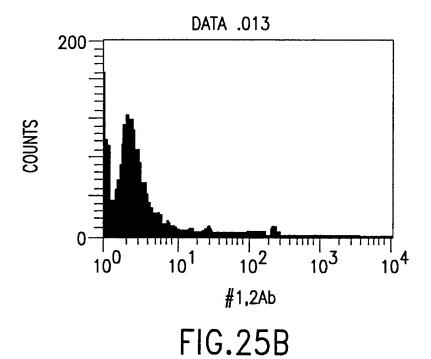


FIG.24





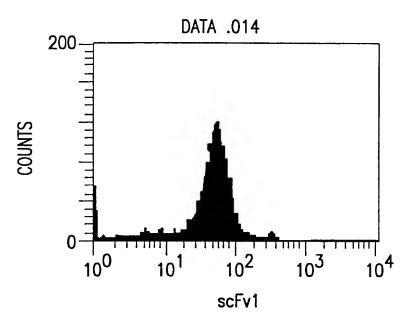


FIG.25C

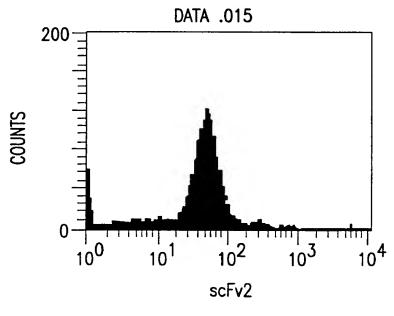


FIG.25D

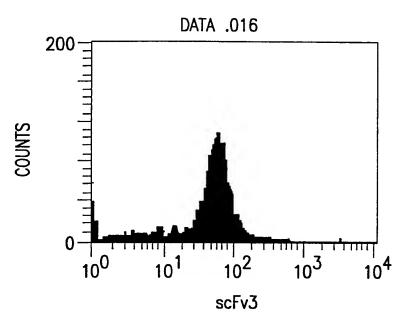


FIG.25E

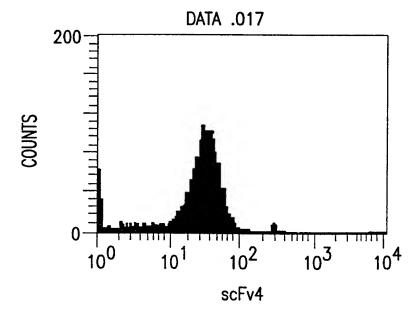
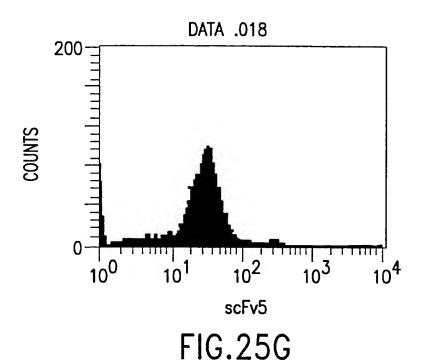
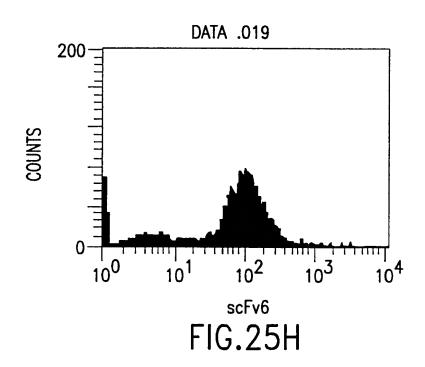


FIG.25F





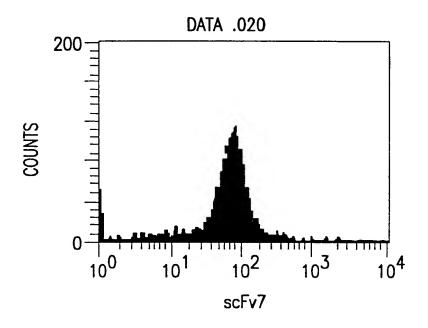


FIG.251

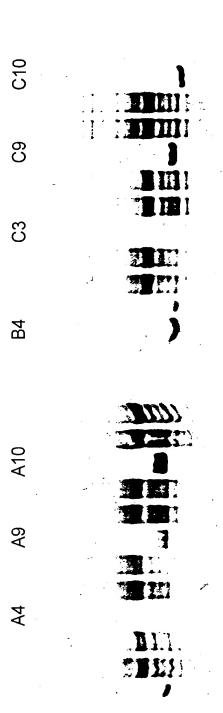


FIG.26

